

LAB 6 :

Visualization and analysis of functional gene networks using Cytoscape



Data used in the network

1. Network : HumanNet v.1

a probabilistic functional gene network of 18,714 validated encoding genes of *Homo sapiens*. (Insuk *et al*, 2011)

We used subset of the network: 'breast cancer related genes'

2. Expression data: RNA-seq data

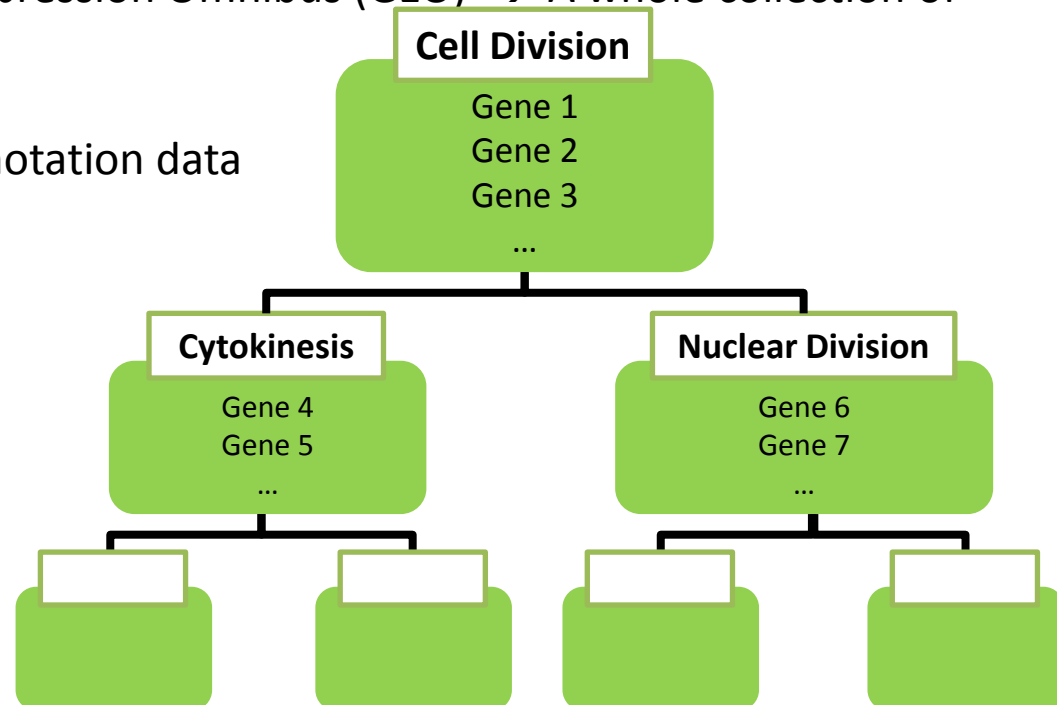
Samples are from 3 Breast cancer patients and 3 normal .

Breast cancer patients have specific type of cancer : Triple Negative Breast Cancer
Data downloaded from : Gene Expression Omnibus (GEO) → A whole collection of various expression data

3. Gene Ontology : Gene-Function annotation data

Described in 3 domains

- Molecular Function
- Cellular Component
- **Biological Process**



Report

Assignment : Draw given Network with Cytoscape on your own.

Things to include

1. Date of the experiment and the day (Tue, Wed, Thur, Fri)
2. Results with “figures of your own” (**1 network file with gradient color, 1 with BINGO output**)
3. Discussion
4. References

Discussion should include :

- What the network visualization tells you.
(What information does the network give you? What can you tell from the expression data and function enrichment analysis using Bingo? → No correct answer for this. Just write what you think)
- Other type of visualization may give you additional points. If you have made modifications, describe what you have done in the report

Data to draw the network can be found in : www.netbiolab.org → teaching

Find Cytoscape at : www.cytoscape.org

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Due date : BTE3601-01-00: 2015.04.28 / BTE3601-02-00: 2015.04.29

BTE3601-03-00: 2015.04.30 / BTE3601-04-00: 2015.05.01

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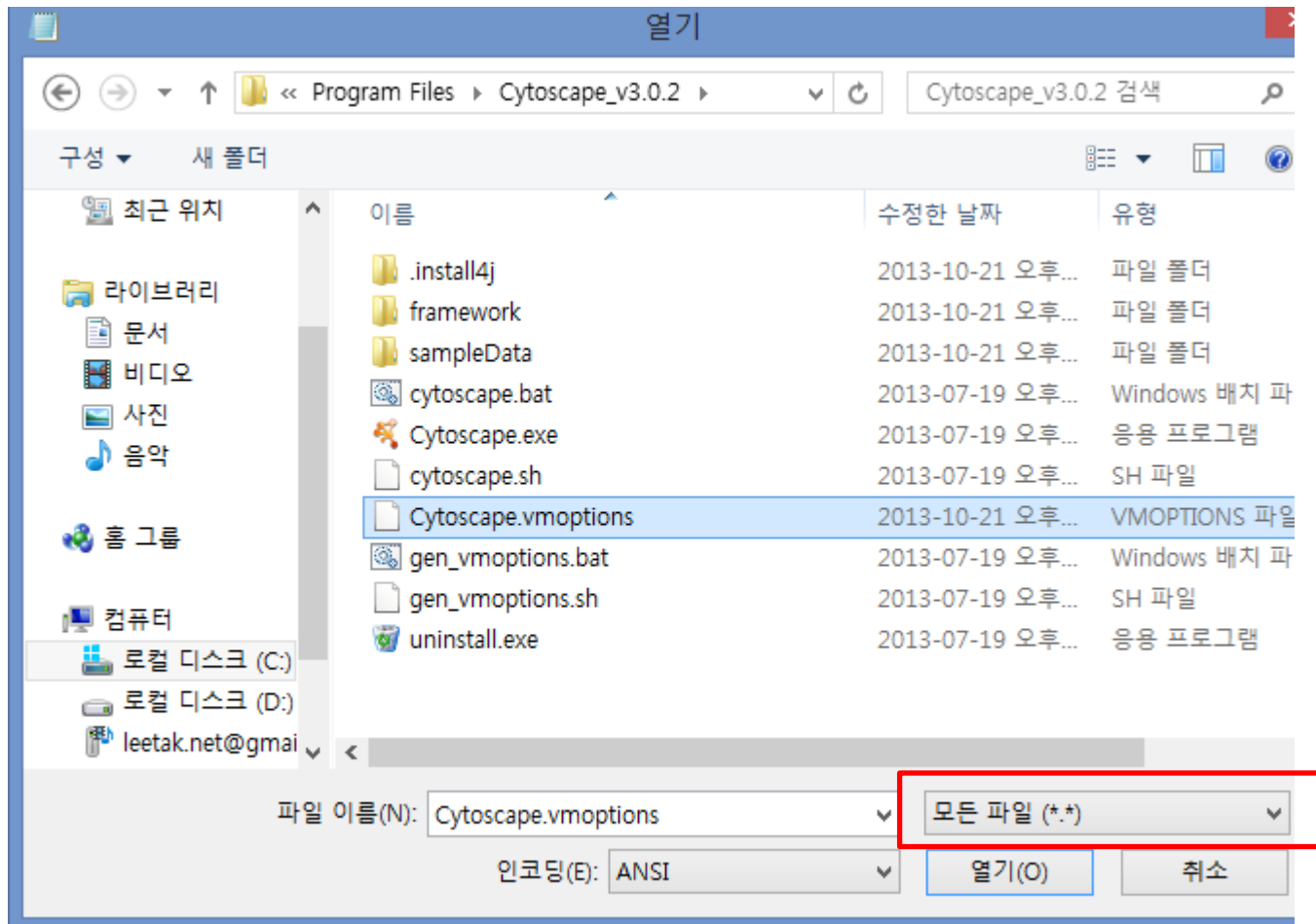
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자바 충돌 문제 해결

메모장을 “관리자 권한”으로 실행

파일 → 열기 → cytoscape 파일 → Cytoscape_vmoptions 파일을 열기



모든 파일 선택

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-Xmx1250m 을 -Xmx512m으로 수정하여 저장

내용 보강

Usage for BiNGO application

Using the file to install BINGO and running it.

1. Apps → App manager → install from file (lower left) → Select “BiNGO jar”

2. Running BiNGO

1) Select all genes in the network (Ctrl + A)

2) Apps → BiNGO

3) BiNGO settings

Type cluster name : any names

Select ontology file : → custom : “ file gene_ontology_ext.obo”

Select namespace → ---

Select organism/annotation → custom “ file : GOBP.BiNGO.txt”

3. start BiNGO. It will take some time.